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RAW SEQUENCE LISTING
PATENT APPLICATION US/09/408,905

DATE: 10/12/1999
TIME: 11:18:47

Input Set: I408905.RAW

This Raw Listing contains the General Information
Section and up to first 5 pages.

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1  <110> APPLICANT: St. Elizabeth's Medical Center of Boston, Inc.
2      Walsh, Kenneth
3  <120> TITLE OF INVENTION: AKT COMPOSITIONS FOR ENHANCING SURVIVAL
4      OF CELLS
5  <130> FILE REFERENCE: S1237/7011/ERP/KA
6  <140> CURRENT APPLICATION NUMBER: US/09/408,905
7  <141> CURRENT FILING DATE: 1999-09-29
8  <150> EARLIER APPLICATION NUMBER: US 60/102,740
9  <151> EARLIER FILING DATE: 1998-10-02
10 <160> NUMBER OF SEQ ID NOS: 8
11 <170> SOFTWARE: FastSEQ for Windows Version 3.0
12 <210> SEQ ID NO 1
13 <211> LENGTH: 2610
14 <212> TYPE: DNA
15 <213> ORGANISM: Homo Sapiens
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19      ggctgtggcc aggccagctg ggctcgggga gcgccagcct gagaggagcg cgtgagcgctc      180
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22      ttcataggct acaaggagcg gccgcaggat gtggaccaac gtgaggctcc cctcaacaac      360
23      ttctctgtgg cgcagtgccg gctgatgaag acggagcggc cccggcccaa caccttcac      420
24      atccgctgcc tgcagtggac cactgtcatc gaacgcacct tccatgtgga gactcctgag      480
25      gagcgggagg agtggacaac cgccatccag actgtggctg acggcctcaa gaagcaggag      540
26      gaggaggaga tggacttccg gtcgggctca cccagtgaca actcaggggc tgaagagatg      600
27      gaggtgtccc tggccaagcc caagcaccgc gtgaccatga acgagtttga gtacctgaag      660
28      ctgctgggca agggcacttt cggcaagggtg atcctgggtga aggagaaggc cacaggccgc      720
29      tactacgcca tgaagatcct caagaaggaa gtcacgtggt ccaaggacga ggtggccac      780
30      aactcaccg agaaccgcgt cctgcagaac tccaggcacc ccttcctcac agccctgaag      840
31      tactctttcc agaccacga ccgcctctgc tttgtcatgg agtacgcaa cgggggagag      900
32      ctgttcttcc acctgtcccg ggaacgtgtg ttctccgagg accgggcccg cttctatggc      960
33      gctgagattg tgtcagccct ggactacctg cactcggaga agaactgtgt gtaccgggac      1020
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35      ctgtgcaagg aggggatcaa ggacggtgcc accatgaaga ccttttgagg cacacctgag      1140
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47      accctcccc gcagcggggt agggaaagaaa actatcctgc gggttttaat ttatttcac      1860
48      cagtttggtc tccgggtgtg gcctcagccc tcagaacaat ccgattcacg tagggaaatg      1920
49      ttaaggactt ctacagctat gcgcaatgtg gcattggggg gccgggcagg tcctgccc      1980
50      gtgtccctc actctgtcag ccagccgccc tgggctgtct gtcaccagct atctgtcatc      2040
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53      cgtgtctctg aggacgtcat cggaggctgg gccctggga tgggaccagg gatgggggat      2220
54      gggccagggt ttaccagtg ggacagagga gcaaggttta aatttgttat tgtgtattat      2280
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56      ccttctgtgt cacagtctt ggtgactgtc ccaccggagc ctccccctca gatgatctct      2400
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61 <210> SEQ ID NO 2

62 <211> LENGTH: 480

63 <212> TYPE: PRT

64 <213> ORGANISM: Homo Sapiens

65 <220> FEATURE:

66 <221> NAME/KEY: DOMAIN

67 <222> LOCATION: (5)...(108)

68 <223> OTHER INFORMATION: Pleckstrin Homology

69 <220> FEATURE:

70 <221> NAME/KEY: DOMAIN

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72 <223> OTHER INFORMATION: Serine-Threonine Kinase

73 <400> SEQUENCE: 2

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77      20          25          30
78      Gly Thr Phe Ile Gly Tyr Lys Glu Arg Pro Gln Asp Val Asp Gln Arg
79      35          40          45
80      Glu Ala Pro Leu Asn Asn Phe Ser Val Ala Gln Cys Gln Leu Met Lys
81      50          55          60
82      Thr Glu Arg Pro Arg Pro Asn Thr Phe Ile Ile Arg Cys Leu Gln Trp
83      65          70          75          80
84      Thr Thr Val Ile Glu Arg Thr Phe His Val Glu Thr Pro Glu Glu Arg
85      85          90          95
86      Glu Glu Trp Thr Thr Ala Ile Gln Thr Val Ala Asp Gly Leu Lys Lys
87      100         105         110
88      Gln Glu Glu Glu Glu Met Asp Phe Arg Ser Gly Ser Pro Ser Asp Asn
89      115         120         125
90      Ser Gly Ala Glu Glu Met Glu Val Ser Leu Ala Lys Pro Lys His Arg
91      130         135         140
92      Val Thr Met Asn Glu Phe Glu Tyr Leu Lys Leu Leu Gly Lys Gly Thr
93      145         150         155         160
94      Phe Gly Lys Val Ile Leu Val Lys Glu Lys Ala Thr Gly Arg Tyr Tyr

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145      gaagtcacg tggccaagga cgaggtggcc cacacactca ccgagaaccg cgtccagcag      420
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147      tgctttgtca tggagtacgc caacgggggc gagctgttct tccacctgtc ccgggagcgt      540
148      gtgttcgccc aggaccgggc ccgcttctat ggcgctgaga ttgtgtcagc cctggactac      600
149      ctgcactcgg agaagaacgt ggtgtaccgg gacctcaagc tggagaacct catgctggac      660
150      aaggacgggc acattaagat cacagacttc gggctgtgca aggaggggat caaggacggt      720
151      gccaccatga agaccttttg cggcacacct gactacctgg ccccgaggt gctggaggac      780
152      aatgactacg gccgtgcagt ggactggtgg gggctggcgg tggtcagtga cgagatgatg      840
153      tgcggtcgcc tgcccttcta caaccaggac catgagaagc tttttgagct catcctcatg      900
154      gaggagatcc gcttcccgcg cacgcttggt cccgaggcca agtccttgct ttcagggctg      960
155      ctcaagaagg accccaagca gaggcttggc ggggctccg aggacgcca ggagatcatg      1020
156      cagcatcgct tctttaccgg tategtgtgg cagcacgtgt acgagaagaa gctcagccca      1080
157      cccttcaagc cccaggtcac gtcggagact gacaccaggt attttgatga ggagttcacg      1140
158      gcccatatga tcaccatcac accacctgac caagatgaca gcatggagtg tgtggacagc      1200
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161      <211> LENGTH: 417
162      <212> TYPE: PRT
163      <213> ORGANISM: Homo Sapiens
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167      Gln Trp Thr Thr Val Ile Glu Arg Thr Phe His Val Glu Thr Pro Glu
168      20          25          30
169      Glu Arg Glu Glu Trp Thr Thr Ala Ile Gln Thr Val Ala Asp Gly Leu
170      35          40          45
171      Lys Lys Gln Glu Glu Glu Met Asp Phe Arg Ser Gly Ser Pro Ser
172      50          55          60
173      Asp Asn Ser Gly Ala Glu Glu Met Glu Val Ser Leu Ala Lys Pro Lys
174      65          70          75          80
175      His Arg Val Thr Met Asn Glu Phe Glu Tyr Leu Lys Leu Leu Gly Lys
176      85          90          95
177      Gly Thr Phe Gly Lys Val Ile Leu Val Lys Glu Lys Ala Thr Ala Tyr
178      100         105         110
179      Tyr Ala Met Lys Ile Leu Lys Lys Glu Val Ile Val Ala Lys Asp Glu
180      115         120         125
181      Val Ala His Thr Leu Thr Glu Asn Arg Val Gln Gln Asn Ser Arg His
182      130         135         140
183      Pro Phe Leu Thr Arg Leu Lys Tyr Ser Phe Gln Thr His Asp Arg Leu
184      145         150         155         160
185      Cys Phe Val Met Glu Tyr Ala Asn Gly Gly Glu Leu Phe Phe His Leu
186      165         170         175
187      Ser Arg Glu Arg Val Phe Ala Glu Asp Arg Ala Arg Phe Tyr Gly Ala
188      180         185         190
189      Glu Ile Val Ser Ala Leu Asp Tyr Leu His Ser Glu Lys Asn Val Val
190      195         200         205
191      Tyr Arg Asp Leu Lys Leu Glu Asn Leu Met Leu Asp Lys Asp Gly His
192      210         215         220
193      Ile Lys Ile Thr Asp Phe Gly Leu Cys Lys Glu Gly Ile Lys Asp Gly
194      225         230         235         240

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195	Ala Thr Met Lys Thr Phe Cys Gly Thr Pro Glu Tyr Leu Ala Pro Glu
196	245 250 255
197	Val Leu Glu Asp Asn Asp Tyr Gly Arg Ala Val Asp Trp Trp Gly Leu
198	260 265 270
199	Gly Val Val Met Tyr Glu Met Met Cys Gly Arg Leu Pro Phe Tyr Asn
200	275 280 285
201	Gln Asp His Glu Lys Leu Phe Glu Leu Ile Leu Met Glu Glu Ile Arg
202	290 295 300
203	Phe Pro Arg Thr Leu Gly Pro Glu Ala Lys Ser Leu Leu Ser Gly Leu
204	305 310 315 320
205	Leu Lys Lys Asp Pro Lys Gln Arg Leu Gly Gly Gly Ser Glu Asp Ala
206	325 330 335
207	Lys Glu Ile Met Gln His Arg Phe Phe Thr Gly Ile Val Trp Gln His
208	340 345 350
209	Val Tyr Glu Lys Lys Leu Ser Pro Pro Phe Lys Pro Gln Val Thr Ser
210	355 360 365
211	Glu Thr Asp Thr Arg Tyr Phe Asp Glu Glu Phe Thr Ala Gln Met Ile
212	370 375 380
213	Thr Ile Thr Pro Pro Asp Gln Asp Asp Ser Met Glu Cys Val Asp Ser
214	385 390 395 400
215	Glu Arg Arg Pro His Phe Pro Gln Phe Ser Tyr Ser Pro Ser Ala Thr
216	405 410 415
217	Ala

<210> SEQ ID NO 5

<211> LENGTH: 2626

<212> TYPE: DNA

<213> ORGANISM: Mus Musculus

<400> SEQUENCE: 5

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225	cgggatgcgg agcggcgggc gcccgaggcc gcggcccggc taggcccagt cgcccgcacg	180
226	cggcggcccc acgctgcggc caggccggct gggctcagcc taccgagaag agactctgat	240
227	catcatccct gggttacccc tgtctctggg ggccacggat accatgaacg acgtagccat	300
228	tgtgaaggag ggctggctgc acaaacgagg ggaatatatt aaaacctggc ggccacgcta	360
229	cttcctcctc aagaacgatg gcacctttat tggctacaag gaacggcctc aggatgtgga	420
230	tcagcgagag tccccactca acaacttctc agtggcacia tgccagctga tgaagacaga	480
231	gcggccaagg cccaacacct ttatcatccg ctgcctgcag tggaccacag tcattgagcg	540
232	caccttccat gtggaaacgc ctgaggagcg ggaagaatgg gccaccgcca ttcagactgt	600
233	ggccgatgga ctcaagaggc aggaagaaga gacgatggac ttccgatcag gctcacccag	660
234	tgacaactca ggggctgaag agatggaggt gtccctggcc aagcccaagc accgtgtgac	720
235	catgaacgag tttgagtacc tgaaactact gggcaagggc acctttggga aagtgtattct	780
236	ggtgaaagag aaggccacag gccgctacta tgccatgaag atcctcaaga aggaggtcat	840
237	cgtcgccaag gatgaggttg cccacacgct tactgagaac cgtgtcctgc agaactctag	900
238	gcaccccttc cttacggccc tcaagtactc attccagacc caccgaccgc tctgctttgt	960
239	catggagtat gccaacgggg gcgagctctt cttccacctg tctcgagagc gcgtgttctc	1020
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243	gaagacattc tgcggaacgc cggagtacct ggcccctgag gtgctggagg acaacgacta	1260
244	cggccgtgca gtggactggt gggggctggg cgtgggtcatg tatgagatga tgtgtggccg	1320

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VERIFICATION SUMMARY
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Line ? Error/Warning

Original Text
